

## SEQUENCE LISTING

&lt;110&gt; Takeda Chemical Industries, Ltd.

&lt;120&gt; Novel G Protein Coupled Receptor Protein and Its DNA

&lt;130&gt; 2590W00P

&lt;150&gt; JP 11-041336

&lt;151&gt; 1999-02-19

&lt;150&gt; JP 11-125768

&lt;151&gt; 1999-05-06

&lt;160&gt; 4

&lt;210&gt; 1

&lt;211&gt; 340

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 1

Met Asn Pro Phe His Ala Ser Cys Trp Asn Thr Ser Ala Glu Leu Leu

5

10

15

Asn Lys Ser Trp Asn Lys Glu Phe Ala Tyr Gln Thr Ala Ser Val Val

20

25

30

Asp Thr Val Ile Leu Pro Ser Met Ile Gly Ile Ile Cys Ser Thr Gly

35

40

45

Leu Val Gly Asn Ile Leu Ile Val Phe Thr Ile Ile Arg Ser Arg Lys

50

55

60

Lys Thr Val Pro Asp Ile Tyr Ile Cys Asn Leu Ala Val Ala Asp Leu

65

70

75

80

Val His Ile Val Gly Met Pro Phe Leu Ile His Gln Trp Ala Arg Gly

85

90

95

Gly Glu Trp Val Phe Gly Gly Pro Leu Cys Thr Ile Ile Thr Ser Leu

100	105	110	
Asp Thr Cys Asn Gln Phe Ala Cys Ser Ala Ile Met Thr Val Met Ser			
115	120	125	
Val Asp Arg Tyr Phe Ala Leu Val Gln Pro Phe Arg Leu Thr Arg Trp			
130	135	140	
Arg Thr Arg Tyr Lys Thr Ile Arg Ile Asn Leu Gly Leu Trp Ala Ala			
145	150	155	160
Ser Phe Ile Leu Ala Leu Pro Val Trp Val Tyr Ser Lys Val Ile Lys			
165	170	175	
Phe Lys Asp Gly Val Glu Ser Cys Ala Phe Asp Leu Thr Ser Pro Asp			
180	185	190	
Asp Val Leu Trp Tyr Thr Leu Tyr Leu Thr Ile Thr Thr Phe Phe Phe			
195	200	205	
Pro Leu Pro Leu Ile Leu Val Cys Tyr Ile Leu Ile Leu Cys Tyr Thr			
210	215	220	
Trp Glu Met Tyr Gln Gln Asn Lys Asp Ala Arg Cys Cys Asn Pro Ser			
225	230	235	240
Val Pro Lys Gln Arg Val Met Lys Leu Thr Lys Met Val Leu Val Leu			
245	250	255	
Val Val Val Phe Ile Leu Ser Ala Ala Pro Tyr His Val Ile Gln Leu			
260	265	270	
Val Asn Leu Gln Met Glu Gln Pro Thr Leu Ala Phe Tyr Val Gly Tyr			
275	280	285	
Tyr Leu Ser Ile Cys Leu Ser Tyr Ala Ser Ser Ser Ile Asn Pro Phe			
290	295	300	
Leu Tyr Ile Leu Leu Ser Gly Asn Phe Gln Lys Arg Leu Pro Gln Ile			
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Gln Arg Arg Ala Thr Glu Lys Glu Ile Asn Asn Met Gly Asn Thr Leu

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330

335

Lys Ser His Phe

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<213> Human

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ATTGGGATTA TCTGTTCAAC AGGGCTGGTT GGCAACATCC TCATTGTATT CACTATAATA	180
AGATCCAGGA AAAAAACAGT CCCTGACATC TATATCTGCA ACCTGGCTGT GGCTGATTTG	240
GTCCACATAG TTGGAATGCC TTTTCTTATT CACCAATGGG CCCGAGGGGG AGAGTGGGTG	300
TTTGGGGGGC CTCTCTGCAC CATCATCACA TCCCTGGATA CTTGTAACCA ATTTGCCTGT	360
AGTGCCATCA TGA CTGTAAT GAGTGTGGAC AGGTACTTTG CCCTCGTCCA ACCATTTCTGA	420
CTGACACGTT GGAGAACAAG GTACAAGACC ATCCGGATCA ATTTGGGCCT TTGGGCAGCT	480
TCCTTTATCC TGGCATTGCC TGTCTGGGTC TACTCGAAGG TCATCAAATT TAAAGACGGT	540
GTTGAGAGTT GTGCTTTTGA TTTGACATCC CCTGACGATG TACTCTGGTA TACACTTTAT	600
TTGACGATAA CAACTTTTTT TTTCCCTCTA CCCTTGATTT TGGTGTGCTA TATTTTAATT	660
TTATGCTATA CTTGGGAGAT GTATCAACAG AATAAGGATG CCAGATGCTG CAATCCCAGT	720
GTACCAAAAC AGAGAGTGAT GAAGTTGACA AAGATGGTGC TGGTGCTGGT GGTAGTCTTT	780
ATCCTGAGTG CTGCCCCCTA TCATGTGATA CAACTGGTGA ACTTACAGAT GGAACAGCCC	840
AACTGGCCT TCTATGTGGG TTATTACCTC TCCATCTGTC TCAGCTATGC CAGCAGCAGC	900
ATTAACCCTT TTCTCTACAT CCTGCTGAGT GGAAATTTCC AGAAACGTCT GCCTCAAATC	960
CAAAGAAGAG CGACTGAGAA GGAAATCAAC AATATGGGAA AACTCTGAA ATCACACTTT	1020
TAG	1023

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ATGAATCCAT TTCATGCATC TTGT

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CTAAAAGTGT GATTCAGAG TGTTT

25

( )